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                          GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          January 17, 2007, 16:29:19 ; Search time 6370.22 Seconds
                                             (without alignments)
                                 10058.575 Million cell updates/sec


Title:           US-10-814-760A-2
Perfect score:   1002
Sequence:        1 gcggagggagtggaaggctc..........cagtacatattggaggggcg 1002


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


Searched:        6366136 seqs, 31973710525 residues


Total number of hits satisfying chosen parameters:     12732272


Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                             PoMC

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1002	100.0	1002	14	BOVPOMC7	J00021 Bovine proo
2	840.8	83.9	1083	14	BTBLPH	V00107 Bovine mRNA
3	838.6	83.7	1084	14	BOVACTH	M25587 Bovine cort
4	763.2	76.2	793	14	BOVBLPHP	M23814 Bos taurus
5	722.4	72.1	732	14	BOVPOMCFR	M38606 Bovine proo
6	629.8	62.9	792	14	OAR507201	AJ507201 Ovis arie
7	570.6	56.9	1097	14	SSPOM1	X00135 Porcine pro
8	570	56.9	1042	14	SSPOMCR	X03561 Pig mRNA fo
9	537.4	53.6	995	14	S73519	S73519 pro-opiomel
10	463.4	46.2	8658	5	HSACTH	V01510 H.sapiens g

	11	462.4	46.1	1230	5	HUMPOMC9	J00292 Human proop
c	12	462.4	46.1	95214	5	AC012457	AC012457 Homo sapi
	13	457.8	45.7	1115	5	MACPOMCA	M19658 Macaca neme
	14	457	45.6	1078	5	BC065832	BC065832 Homo sapi
	15	456	45.5	1050	2	CQ720465	CQ720465 Sequence
	16	438.2	43.7	908	5	HUMPOMCZ	M38297 Human proop
	17	432.8	43.2	663	14	AY024339	AY024339 Canis fam
	18	413.4	41.3	804	5	BT019918	BT019918 Homo sapi
	19	413.4	41.3	804	8	AY888671	AY888671 Synthetic
	20	413.2	41.2	936	2	AX534756	AX534756 Sequence
	21	412.4	41.2	804	8	AY893864	AY893864 Synthetic
	22	410.8	41.0	801	5	CR541826	CR541826 Homo sapi
	23	410.8	41.0	804	8	AY893863	AY893863 Synthetic
	24	409	40.8	899	6	S78260	S78260 pro-opiomel
	25	372.6	37.2	1315	2	AX463491	AX463491 Sequence
	26	360.8	36.0	585	14	MVIPOMCA	J03039 M.vison (mi
	27	325	32.4	562	5	AY091991	AY091991 Pan trogl
	28	310.6	31.0	559	5	AY091992	AY091992 Gorilla g
	29	309.8	30.9	237327	12	AC103454	AC103454 Rattus no
c	30	309.8	30.9	250999	12	AC119009	AC119009 Rattus no
	31	309.4	30.9	845	2	AR373945	AR373945 Sequence
	32	309.4	30.9	845	2	AR474303	AR474303 Sequence
	33	309.4	30.9	845	6	MUSPOMC03	J00612 Mouse proop
	34	309.4	30.9	211926	6	AC111092	AC111092 Mus muscu
	35	309	30.8	759	6	MMOPI2	V01529 Mouse gene
	36	308.2	30.8	781	6	RATPOMC3	J00759 Rat proopio
	37	307.2	30.7	1070	6	BC061215	BC061215 Mus muscu
	38	306.8	30.6	967	6	BC058443	BC058443 Rattus no
	39	303	30.2	714	6	AF510391	AF510391 Rattus no
	40	299.4	29.9	301	7	BV104815	BV104815 MARC 6319
	41	297	29.6	708	2	AX534751	AX534751 Sequence
	42	271.6	27.1	496	5	AY091993	AY091993 Pongo pyg
	43	271	27.0	490	5	AY091994	AY091994 Macaca sp
	44	267.8	26.7	490	5	AY091995	AY091995 Saguinus
	45	244.8	24.4	256	14	S57982	S57982 proopiomela

ALIGNMENTS

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RESULT 1
BOVPOMC7
LOCUS       BOVPOMC7                 1002 bp    DNA    linear    MAM 30-OCT-1994
DEFINITION  Bovine proopiomelanocortin (POMC) gene, exon 3.
ACCESSION   J00021
VERSION     J00021.1  GI:163568
KEYWORDS    adrenocorticotropin; alpha-melanotropin; beta-lipotropin;
            beta-melanotropin; corticotropin; enkephalin; gamma-lipotropin;
            lipotropin; melanotropin; met-enkephalin; neuropeptide Y;
            proopiomelanocortin.
SEGMENT     7 of 7
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 100 to 936)
  AUTHORS   Nakanishi,S., Inoue,A., Kita,T., Nakamura,M., Chang,A.C.,
            Cohen,S.N. and Numa,S.
  TITLE     Nucleotide sequence of cloned cDNA for bovine
            corticotropin-beta-lipotropin precursor
  JOURNAL   Nature 278 (5703), 423-427 (1979)
  PUBMED    221818
REFERENCE   2  (bases 82 to 140; 889 to 962)
  AUTHORS   Nakanishi,S., Teranishi,Y., Noda,M., Notake,M., Watanabe,Y.,
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                      Kakidani,H., Jingami,H. and Numa,S.
    TITLE             The protein-coding sequence of the bovine ACTH-beta-LPH precursor
                      gene is split near the signal peptide region
    JOURNAL           Nature 287 (5784), 752-755 (1980)
    PUBMED            6253815
 REFERENCE           3  (bases 1 to 1002)
    AUTHORS           Nakanishi,S., Teranishi,Y., Watanabe,Y., Notake,M., Noda,M.,
                      Kakidani,H., Jingami,H. and Numa,S.
    TITLE             Isolation and characterization of the bovine
                      corticotropin/beta-lipotropin precursor gene
    JOURNAL           Eur. J. Biochem. 115 (3), 429-438 (1981)
    PUBMED            6263630
 COMMENT             Original source text: Bovine calf thymus DNA [2],[3] and cDNA to
                      mRNA [1].
                      The POMC gene region is approximately 7.3 kb in length, coding for
                      corticotropin (ACTH), beta-lipotropin (beta-LPH) and their
                      component peptides which independently possess biological activity.
                      The region consists of three exons divided by two large introns.
                      Repetitive sequences are found in the 5' flanking segment and in
                      each of the introns. Exon 3, according to [2], contains the gene
                      sequence for most of the protein structure, including the known
                      biologically active component peptides. [1] reports the boundaries
                      of the mature peptides.
 FEATURES                     Location/Qualifiers
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                              /protein_id="AAB59262.1"
                              /db_xref="GI:163570"
                              /translation="MPRLCSSRSGALLLALLLQASMEVRGWCLESSQCQDLTTESNLL
                              ACIRACKPDLSAETPVFPGNGDEQPLTENPRKYVMGHFRWDRFGRRNGSSSSGVGGAA
                              QKREEEVAVGEGPGPRGDDAETGPREDKRSYSMEHFRWGKPVGKKRRPVKVYPNGAED
                              ESAQAFPLEFKRELTGERLEQARGPEAQAESAAARAELEYGLVAEAEAEAAEKKDSGP
                              YKMEHFRWGSPPKDKRYGGFMTSEKSQTPLVTLFKNAIIKNAHKKGQ"
     mat_peptide              195. .230
                              /gene="POMC"
                              /product="gamma-melanotropin (gamma-MSH)"
     mat_peptide              360. .476
                              /gene="POMC"
                              /product="corticotropin (ACTH)"
     mat_peptide              360. .398
                              /gene="POMC"
                              /product="alpha-melanotropin (alpha-MSH)"
     mat_peptide              411. .476
                              /gene="POMC"
                              /product="corticotropin-like intermediate peptide (CLIP)"
     mat_peptide              483. .761
                              /gene="POMC"
                              /product="beta-lipotropin (beta-LPH)"
     mat_peptide              483. .662
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                              /product="gamma-lipotropin (gamma-LPH)"
     mat_peptide              606. .662
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     mat_peptide              669. .761
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                              /product="beta-endorphin (beta-EP)"
     mat_peptide              669. .683
                              /gene="POMC"
                              /product="met-enkephalin (met-EK)"
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                          /number=2
          conflict        83
                          /citation=[2]
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ORIGIN        about 420 bp after <bovpomc6>; 57 bp upstream of BstNI site.
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Best Local Similarity   100.0%;   Pred. No. 2.4e-249;
Matches 1002; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 GCGGAGGGAGTGGAAGGCTCAGGCGGCGCGCTTGAGGGGCGGGTGAACGCCGCGGCCTGG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGGAGGGAGTGGAAGGCTCAGGCGGCGCGCTTGAGGGGCGGGTGAACGCCGCGGCCTGG 60

Qy     61 AGTGGGCGGGGCCTGACGCGCTCTGCCGCTCTCCGCAGGCGTGCATCCGGGCCTGCAAGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGGGCGGGGCCTGACGCGCTCTGCCGCTCTCCGCAGGCGTGCATCCGGGCCTGCAAGC 120

Qy    121 CCGACCTCTCCGCCGAGACGCCGGTGTTCCCCGGCAACGGCGATGAGCAGCCGCTGACTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGACCTCTCCGCCGAGACGCCGGTGTTCCCCGGCAACGGCGATGAGCAGCCGCTGACTG 180

Qy    181 AGAACCCCCGGAAGTACGTCATGGGCCATTTCCGCTGGGACCGCTTCGGCCGTCGGAATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGAACCCCCGGAAGTACGTCATGGGCCATTTCCGCTGGGACCGCTTCGGCCGTCGGAATG 240

Qy    241 GTAGCAGCAGCAGCGGAGTTGGGGGCGCGGCCCAGAAGCGCGAGGAGGAAGTGGCGGTGG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGCAGCAGCAGCGGAGTTGGGGGCGCGGCCCAGAAGCGCGAGGAGGAAGTGGCGGTGG 300

Qy    301 GCGAAGGCCCCGGGCCCCGCGGCGATGACGCCGAGACGGGTCCGCGCGAGGACAAGCGTT 360
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Db    301 GCGAAGGCCCCGGGCCCCGCGGCGATGACGCCGAGACGGGTCCGCGCGAGGACAAGCGTT 360

Qy    361 CTTACTCCATGGAACACTTCCGCTGGGGCAAGCCGGTGGGCAAGAAGCGGCGCCCGGTGA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTACTCCATGGAACACTTCCGCTGGGGCAAGCCGGTGGGCAAGAAGCGGCGCCCGGTGA 420
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Qy    421 AGGTGTACCCCAACGGCGCCGAGGACGAGTCGGCCCAGGCCTTTCCCCTCGAATTCAAGA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGTGTACCCCAACGGCGCCGAGGACGAGTCGGCCCAGGCCTTTCCCCTCGAATTCAAGA 480

Qy    481 GGGAGCTGACCGGGGAGAGGCTCGAGCAGGCGCGCGGCCCCGAGGCCCAGGCTGAGAGTG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGGAGCTGACCGGGGAGAGGCTCGAGCAGGCGCGCGGCCCCGAGGCCCAGGCTGAGAGTG 540

Qy    541 CGGCCGCCCGGGCTGAGCTGGAGTATGGCCTGGTGGCGGAGGCGGAGGCTGAGGCGGCCG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGGCCGCCCGGGCTGAGCTGGAGTATGGCCTGGTGGCGGAGGCGGAGGCTGAGGCGGCCG 600

Qy    601 AGAAGAAGGACTCGGGGCCCTATAAGATGGAACACTTCCGCTGGGGCAGCCCGCCCAAGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    661 ACAAGCGCTACGGCGGGTTCATGACCTCCGAGAAGAGCCAAACGCCCCTTGTCACGCTGT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACAAGCGCTACGGCGGGTTCATGACCTCCGAGAAGAGCCAAACGCCCCTTGTCACGCTGT 720

Qy    721 TCAAAAACGCCATCATCAAGAACGCCCACAAGAAGGGCCAGTGAGGGCGCAGCGGGCAGG 780
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Db    721 TCAAAAACGCCATCATCAAGAACGCCCACAAGAAGGGCCAGTGAGGGCGCAGCGGGCAGG 780

Qy    781 GGCCTCTCTCCGCGGAAAGTTGACCCTGAAGGCCTCTCTTCTGCCCTCCTACCGCCTCGC 840
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Db    781 GGCCTCTCTCCGCGGAAAGTTGACCCTGAAGGCCTCTCTTCTGCCCTCCTACCGCCTCGC 840

Qy    841 AGCCTGGGTGAGGATTCGCCCAGGCAGTGATGGCGCCAGGTATCCCGACTCTTAAAGCTG 900
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Db    841 AGCCTGGGTGAGGATTCGCCCAGGCAGTGATGGCGCCAGGTATCCCGACTCTTAAAGCTG 900

Qy    901 TCTGTAGTTAAGAAATAAAACCTTTCAAGTTTCACGAATATTGACTGGGTGAATTAAAAA 960
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Qy    961 CGCATTTCCATCAAGTAAAGGGCAGTACATATTGGAGGGGCG 1002
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